SEQUENCE LISTING

<110> Universite Liege

<120> Hybrid proteins of active-site serine ß-lactamase

<130> 2002-24

<140>
<141>

<150> EP 04 075 430.1
<151> 2004-02-11

<160> 41

<170> PatentIn Ver. 2.1

<210> 1
<211> 858
<212> DNA
<213> Escherichia coli

<220>
<223> ß-lactamase TEM-1 gene (complementary strand)

<400> 1
ccaatgctta atcagtgagg cacctatctc agcgatctgt ctatttcgtt catccatagt 60
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tgctgcaatg ataccgcgag acccacgctc accggctcca gatttatcag caataaacca 180
gccagccgga agggccgagc gcagaagtgg tcctgcaact ttatccgcct ccatccagtc 240
tattaattgt tgccgggaag ctagagtaag tagttcgcca gttaatagtt tgcgcaacgt 300
tgttgccatt gctgcaggca tcgtggtgtc acgctcgtcg tttggtatgg cttcattcag 360
ctccggttcc caacgatcaa ggcgagttac atgatccccc atgttgtgca aaaaagcggt 420
tagctccttc ggtcctccga tcgttgtcag aagtaagttg gccgcagtgt tatcactcat 480
ggttatggca gcactgcata attctcttac tgtcatgcca tccgtaagat gcttttctgt 540
gactggtgag tactcaacca agtcattctg agaatagtgt atgcggcgac cgagttgctc 600
ttgcccggcg tcaacacggg ataataccgc gccacatagc agaactttaa aagtgctcat 660
cattggaaaa cgttcttcgg ggcgaaaact ctcaaggatc ttaccgctgt tgagatccag 720
ttcgatgtaa cccactcgtg cacccaactg atcttcagca tcttttactt tcaccagcgt 780
ttctgggtga gcaaaaacag gaaggcaaaa tgccgcaaaa aagggaataa gggcgacacg 840
gaaatgttga atactcat 858

<210> 2
<211> 921
<212> DNA
<213> Bacillus licheniformis

<220>
<223> ß-lactamase BlaP gene

<400> 2
atgaaattat ggttcagtac tttaaaactg aaaaaggctg cagcagtgtt gcttttctct 60
tgcgtcgcgc ttgcaggatg cgctaacaat caaacgaatg cctcgcaacc tgccgagaag 120
aatgaaaaga cggagatgaa agatgatttt gcaaaacttg aggaacaatt tgatgcaaaa 180
ctcgggatct ttgcattgga tacaggtaca aaccggacgg tagcgtatcg gccggatgag 240
cgttttgctt ttgcttcgac gattaaggct ttaactgtag gcgtgctttt gcaacagaaa 300
tcaatagaag atctgaacca gagaataaca tatacacgtg atgatcttgt aaactacaac 360
ccgattacgg aaaagcacgt tgatacggga atgacgctca aagagcttgc ggatgcttcg 420
cttcgatata gtgacaatgc ggcacagaat ctcattctta aacaaattgg cggacctgaa 480
agtttgaaaa aggaactgag gaagattggt gatgaggtta caaatcccga acgattcgaa 540
ccagagttaa atgaagtgaa tccgggtgaa actcaggata ccagtacagc aagagcactt 600

gtcacaagcc ttcgagcctt tgctcttgaa gataaacttc caagtgaaaa acgcgagctt 660
ttaatcgatt ggatgaaacg aaataccact ggagacgcct taatccgtgc cggtgtgccg 720
gacggttggg aagtggctga taaaactgga gcggcatcat atggaacccg gaatgacatt 780
gccatcattt ggccgccaaa aggagatcct gtcgttcttg cagtattatc cagcagggat 840
aaaaaggacg ccaagtatga tgataaactt attgcagagg caacaaaggt ggtaatgaaa 900
gccttaaaca tgaacggcaa a 921

<210> 3
<211> 975
<212> DNA
<213> Streptomyces cacaoi

<220>
<223> ß-lactamase BlaL gene

<400> 3
atgcgtatcc gtcccacccg tcgtcttctc ctcggcgcgg tcgcgccgct cgccctcgtt 60
ccgctggtgg cctgcggtca ggcgtcgggc tccgagagcg gccagcagcc cggcctcggc 120
ggttgcggga cgagcgcaca cggctcggcg gacgcccacg agaaggagtt ccgggcgctg 180
gagaagaagt tcgacgccca ccctggcgtc tacgccatcg acacccgcga cggccaggag 240
atcacccacc gggccgacga gcgcttcgcc tacggctcga ccttcaaggc cctccaggcg 300
ggcgcgatcc ttgcgcaagt tctccgagac gggcgcgaag tccggcgggg cgccgaggcc 360
gacggcatgg acaaggtggt ccactacggg caggacgcga tcctgcccaa ctcaccggtg 420
accgagaagc acgtcgcgga cggcatgtcc ctgcgcgagc tgtgcgacgc cgtcgtggcc 480
tacagcgaca acaccgcggc caacctgctc ttcgaccagc tcggcggccg aaggggctca 540
acgcgggtcc tcaagcagct cggcgaccac accacgagca tggaccgcta cgagcaggag 600
ctgggctcgg ccgtccccgg cgacccccgg gacaccagca cgccgcgcgc gttcgccgag 660
gacctgcgcg ccttcgccgt cgaggacggc gagaaggccg ccctcgcgcc caacgaccgc 720
gagcagctga acgactggat gagcgggagc aggaccggcg acgcgctgat ccgggccggt 780
gtgccgaagg actggaaggt ggaggacaag agcggccagg tcaagtacgg cacccggaac 840
gacatcgccg tcgtccgccc gcccggccgc gcgccgatcg tcgtctcggt gatgagccac 900
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gccgacggtc tgaag 975

<210> 4
<211> 286
<212> PRT
<213> Escherichia coli

<220>
<223> ß-lactamase TEM-1

<400> 4
Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1 5 10 15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
65 70 75 80

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
85 90 95

```
Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
            100                 105                 110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
        115                 120                 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
    130                 135                 140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
145                 150                 155                 160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
                165                 170                 175

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
            180                 185                 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
        195                 200                 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
    210                 215                 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
225                 230                 235                 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
                245                 250                 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
            260                 265                 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
        275                 280                 285
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<210> 5
<211> 307
<212> PRT
<213> Bacillus licheniformis

<220>
<223> ß-lactamase BlaP

<400> 5

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Met Lys Leu Trp Phe Ser Thr Leu Lys Leu Lys Lys Ala Ala Ala Val
  1               5                  10                  15

Leu Leu Phe Ser Cys Val Ala Leu Ala Gly Cys Ala Asn Asn Gln Thr
             20                  25                  30

Asn Ala Ser Gln Pro Ala Glu Lys Asn Glu Lys Thr Glu Met Lys Asp
         35                  40                  45

Asp Phe Ala Lys Leu Glu Glu Gln Phe Asp Ala Lys Leu Gly Ile Phe
     50                  55                  60

Ala Leu Asp Thr Gly Thr Asn Arg Thr Val Ala Tyr Arg Pro Asp Glu
 65                  70                  75                  80

Arg Phe Ala Phe Ala Ser Thr Ile Lys Ala Leu Thr Val Gly Val Leu
                 85                  90                  95
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Leu Gln Gln Lys Ser Ile Glu Asp Leu Asn Gln Arg Ile Thr Tyr Thr
            100                 105                 110

Arg Asp Asp Leu Val Asn Tyr Asn Pro Ile Thr Glu Lys His Val Asp
        115                 120                 125

Thr Gly Met Thr Leu Lys Glu Leu Ala Asp Ala Ser Leu Arg Tyr Ser
    130                 135                 140

Asp Asn Ala Ala Gln Asn Leu Ile Leu Lys Gln Ile Gly Gly Pro Glu
145                 150                 155                 160

Ser Leu Lys Lys Glu Leu Arg Lys Ile Gly Asp Glu Val Thr Asn Pro
                165                 170                 175

Glu Arg Phe Glu Pro Glu Leu Asn Glu Val Asn Pro Gly Glu Thr Gln
            180                 185                 190

Asp Thr Ser Thr Ala Arg Ala Leu Val Thr Ser Leu Arg Ala Phe Ala
        195                 200                 205

Leu Glu Asp Lys Leu Pro Ser Glu Lys Arg Glu Leu Leu Ile Asp Trp
    210                 215                 220

Met Lys Arg Asn Thr Thr Gly Asp Ala Leu Ile Arg Ala Gly Val Pro
225                 230                 235                 240

Asp Gly Trp Glu Val Ala Asp Lys Thr Gly Ala Ala Ser Tyr Gly Thr
                245                 250                 255

Arg Asn Asp Ile Ala Ile Ile Trp Pro Pro Lys Gly Asp Pro Val Val
            260                 265                 270

Leu Ala Val Leu Ser Ser Arg Asp Lys Lys Asp Ala Lys Tyr Asp Asp
        275                 280                 285

Lys Leu Ile Ala Glu Ala Thr Lys Val Val Met Lys Ala Leu Asn Met
    290                 295                 300

Asn Gly Lys
305
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<210> 6
<211> 325
<212> PRT
<213> Streptomyces cacaoi

<220>
<223> ß-lactamase BlaL

<400> 6

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Met Arg Ile Arg Pro Thr Arg Arg Leu Leu Leu Gly Ala Val Ala Pro
  1               5                  10                  15

Leu Ala Leu Val Pro Leu Val Ala Cys Gly Gln Ala Ser Gly Ser Glu
             20                  25                  30

Ser Gly Gln Gln Pro Gly Leu Gly Gly Cys Gly Thr Ser Ala His Gly
         35                  40                  45

Ser Ala Asp Ala His Glu Lys Glu Phe Arg Ala Leu Glu Lys Lys Phe
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```
     50                  55                  60

Asp Ala His Pro Gly Val Tyr Ala Ile Asp Thr Arg Asp Gly Gln Glu
 65                  70                  75                  80

Ile Thr His Arg Ala Asp Glu Arg Phe Ala Tyr Gly Ser Thr Phe Lys
                85                  90                  95

Ala Leu Gln Ala Gly Ala Ile Leu Ala Gln Val Leu Arg Asp Gly Arg
            100                 105                 110

Glu Val Arg Arg Gly Ala Glu Ala Asp Gly Met Asp Lys Val Val His
        115                 120                 125

Tyr Gly Gln Asp Ala Ile Leu Pro Asn Ser Pro Val Thr Glu Lys His
    130                 135                 140

Val Ala Asp Gly Met Ser Leu Arg Glu Leu Cys Asp Ala Val Val Ala
145                 150                 155                 160

Tyr Ser Asp Asn Thr Ala Ala Asn Leu Leu Phe Asp Gln Leu Gly Gly
                165                 170                 175

Arg Arg Gly Ser Thr Arg Val Leu Lys Gln Leu Gly Asp His Thr Thr
            180                 185                 190

Ser Met Asp Arg Tyr Glu Gln Glu Leu Gly Ser Ala Val Pro Gly Asp
        195                 200                 205

Pro Arg Asp Thr Ser Thr Pro Arg Ala Phe Ala Glu Asp Leu Arg Ala
    210                 215                 220

Phe Ala Val Glu Asp Gly Glu Lys Ala Ala Leu Ala Pro Asn Asp Arg
225                 230                 235                 240

Glu Gln Leu Asn Asp Trp Met Ser Gly Ser Arg Thr Gly Asp Ala Leu
                245                 250                 255

Ile Arg Ala Gly Val Pro Lys Asp Trp Lys Val Glu Asp Lys Ser Gly
            260                 265                 270

Gln Val Lys Tyr Gly Thr Arg Asn Asp Ile Ala Val Val Arg Pro Pro
        275                 280                 285

Gly Arg Ala Pro Ile Val Val Ser Val Met Ser His Gly Asp Thr Gln
    290                 295                 300

Asp Ala Glu Pro His Asp Glu Leu Val Ala Glu Ala Gly Leu Val Val
305                 310                 315                 320

Ala Asp Gly Leu Lys
                325
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<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7

tcagttaaca atttcaacaa agaacaacaa aatgct 36

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
tcgaaatttt ttgttgtctt cctcttttgg 30

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 9
catatgaaaa agaaaaacat ttattcaatt cgt 33

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
ggatccttat agttcgcgac gacgtccagc taa 33

<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
cgggagctca ggctcaccca gaaacgctgg tg 32

<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
cgggaattct caccaatgct taatcagtga ggcacc 36

<210> 13
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
ggctgtactt acaaattaat ccttaatggt aaaacattg 39

<210> 14
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
ctctctttca gttaccgtaa aggtcttagt cgc 33

<210> 15
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
aggttttatc catacgacgt cccggactac gccacaact 39

<210> 16
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
agttgtggcg tagtccggga cgtcgtatgg ataaaacct 39

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17
ctcgagaaaa gaaatttggt gaatttccac 30

<210> 18
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
gcaacgtgga gtgctccctc tgcagtgttt 30

<210> 19
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
ccgatcatca aacttctcaa gctgcttaaa ctcctgcgcc ggaaacttct caagctgctt 60
aaactcctgc cggatcagga gtttaagcag 90

<210> 20
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
ctgcttaaac tcctgatccg gcaggagttt aagcagcttg agaagtttcc ggcgcaggag 60
tttaagcagc ttgagaagtt tgatgatcgg 90

<210> 21
<211> 54
<212> DNA
<213> Escherichia coli

<220>
<223> STa, heat-stable enterotoxin

<400> 21
aacacgtttt actgctgcga actttgctgc aacccagcat gcgcaggttg ctac 54

<210> 22
<211> 18
<212> PRT
<213> Escherichia coli

<220>
<223> STa, heat-stable enterotoxin

<400> 22
Asn Thr Phe Tyr Cys Cys Glu Leu Cys Cys Asn Pro Ala Cys Ala Gly
1 5 10 15

Cys Tyr

<210> 23
<211> 201
<212> DNA
<213> Staphylococcus aureus

<220>
<223> Protein A, one Fc binding domain

<400> 23
tcagtgaaca atttcaacaa agaacaacaa aatgctttct atgaaatttt acatttacct 60
aacttaactg aagaacaacg taacggcttc atccaaagcc ttaaagacga tccttcagtg 120
agcaaagaaa ttttagcaga agctaaaaag ctaaacgatg ctcaagcacc aaaagaggaa 180
gacaacaaga aaaaatttcg a 201

<210> 24
<211> 67
<212> PRT
<213> Staphylococcus aureus

<220>
<223> Protein A, one Fc binding domain

<400> 24
Ser Val Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Lys Lys
50 55 60

Lys Phe Arg
65

<210> 25
<211> 375
<212> DNA
<213> Staphylococcus aureus

<220>
<223> Protein A, two Fc binding domains

<400> 25
tcagtgaaca atttcaacaa agaacaacaa aatgctttct atgaaatctt gaacatgcct 60
aacttgaacg aagaacaacg caatggtttc atccaaagct taaaagatga cccaagtcaa 120
agtgctaacc ttttagcaga agctaaaaag ttaaatgaat ctcaagcacc gaaagctgat 180
aacaatttca acaaagaaca acaaaatgct ttctatgaaa ttttacattt acctaactta 240
actgaagaac aacgtaacgg cttcatccaa agccttaaag acgatccttc agtgagcaaa 300
gaaattttag cagaagctaa aaagctaaac gatgctcaag caccaaaaga ggaagacaac 360
aagaaaaaat ttcga 375

<210> 26
<211> 125
<212> PRT
<213> Staphylococcus aureus

<220>
<223> Protein A, two Fc binding domains

<400> 26
Ser Val Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn
50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro
85 90 95

Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys Glu Glu Asp Asn Lys Lys Lys Phe Arg
115 120 125

<210> 27
<211> 177
<212> DNA
<213> Streptococcus pyogenes

<220>
<223> Protein G, one Fc binding domain

<400> 27
ggctgtactt acaaattaat ccttaatggt aaaacattga aaggccaaac aactactgaa 60
gctgttgatg ctgctactgc agaaaaagtc ttcaaacaat acgctaacga caacggtgtt 120
gacggtgaat ggacttacga cgatgcgact aagaccttta cggtaactga aagagaa 177

<210> 28
<211> 59
<212> PRT
<213> Streptococcus pyogenes

<220>
<223> Protein G, one Fc binding domain

<400> 28
Gly Cys Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Gln
1 5 10 15

Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys
20 25 30

Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp
35 40 45

Ala Thr Lys Thr Phe Thr Val Thr Glu Arg Glu
50 55

<210> 29
<211> 387
<212> DNA
<213> Streptococcus pyogenes

<220>
<223> Protein G, two Fc binding domains

<400> 29
ggctgtactt acaaattaat ccttaatggt aaaacattga aaggccaaac aactactgaa 60
gctgttgatg ctgctactgc agaaaaagtc ttcaaacaat acgctaacga caacggtgtt 120
gacggtgaat ggacttacga cgatgcgact aagaccttta cagttactga aaaaccagaa 180
gtgatcgatg cgtctgaatt aacaccagcc gtgacaactt acaaacttgt tattaatggt 240
aaaacattga aaggcgaaac aactactaaa gcagtagacg cagaaactgc agaaaaagcc 300
ttcaaacaat acgctaacga caacggtgtt gatggtgttt ggacttatga tgatgcgact 360
aagaccttta cggtaactga aagagag 387

<210> 30
<211> 129
<212> PRT
<213> Streptococcus pyogenes

<220>
<223> Protein G, two Fc binding domains

<400> 30
Gly Cys Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Gln
1 5 10 15

Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys
20 25 30

Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp
35 40 45

Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala
50 55 60

Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly
65 70 75 80

Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala Glu Thr
85 90 95

Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly
100 105 110

Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Arg
115 120 125

Glu

<210> 31
<211> 39
<212> DNA
<213> Influenza virus

<220>

<223> hemagglutinin epitope

<400> 31
aggttttatc catacgacgt cccggactac gccacaact 39

<210> 32
<211> 13
<212> PRT
<213> Influenza virus

<220>
<223> Hemagglutinin epitope

<400> 32
Arg Phe Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Thr Thr
1 5 10

<210> 33
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<223> phospholipase (hPLA2)

<400> 33
ctcgagaaaa gaaatttggt gaatttccac agaatgatca agttgacgac aggaaaggaa 60
gccgcactca gttatggctt ctacggctgc cactgtggcg tgggtggcag aggatccccc 120
aaggatgcaa cggatcgctg ctgtgtcact catgactgtt gctacaaacg tctggagaaa 180
cgtggatgtg gcaccaaatt tctgagctac aagtttagca actcggggag cagaatcacc 240
tgtgcaaaac aggactcctg cagaagtcaa ctgtgtgagt gtgataaggc tgctgccacc 300
tgttttgcta gaaacaagac gacctacaat aaaaagtacc agtactattc caataaacac 360
tgcagaggga gcactccacg ttgc 384

<210> 34
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<223> phospholipase (hPLA2)

<400> 34
Leu Glu Lys Arg Asn Leu Val Asn Phe His Arg Met Ile Lys Leu Thr
1 5 10 15

Thr Gly Lys Glu Ala Ala Leu Ser Tyr Gly Phe Tyr Gly Cys His Cys
20 25 30

Gly Val Gly Gly Arg Gly Ser Pro Lys Asp Ala Thr Asp Arg Cys Cys
35 40 45

Val Thr His Asp Cys Cys Tyr Lys Arg Leu Glu Lys Arg Gly Cys Gly
50 55 60

Thr Lys Phe Leu Ser Tyr Lys Phe Ser Asn Ser Gly Ser Arg Ile Thr
65 70 75 80

Cys Ala Lys Gln Asp Ser Cys Arg Ser Gln Leu Cys Glu Cys Asp Lys
85 90 95

Ala Ala Ala Thr Cys Phe Ala Arg Asn Lys Thr Thr Tyr Asn Lys Lys
100 105 110

Tyr Gln Tyr Tyr Ser Asn Lys His Cys Arg Gly Ser Thr Pro Arg Cys
115 120 125

<210> 35
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: affinity to LPS

<400> 35
ccgatcatca aacttctcaa gctgcttaaa ctcctgcgcc ggaaacttct caagctgctt 60
aaactcctgc cggatcagga gtttaagcag 90

<210> 36
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: affinity to LPS

<400> 36
Pro Ile Ile Lys Leu Leu Lys Leu Leu Lys Leu Leu Arg Arg Lys Leu
1 5 10 15

Leu Lys Leu Leu Lys Leu Leu Pro Asp Gln Glu Phe Lys Gln
20 25 30

<210> 37
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> HA peptide containing linker

<220>
<223> Description of Artificial Sequence: peptide

<400> 37
Gly Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Gly
1 5 10 15

<210> 38
<211> 377
<212> PRT

<213> Escherichia coli

<220>
<223> AmpC ß-lactamse Protein

<400> 38

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Met Phe Lys Thr Thr Leu Cys Ala Leu Leu Ile Thr Ala Ser Cys Ser
  1               5                  10                  15

Thr Phe Ala Ala Pro Gln Gln Ile Asn Asp Ile Val His Arg Thr Ile
             20                  25                  30

Thr Pro Leu Ile Glu Gln Gln Lys Ile Pro Gly Met Ala Val Ala Val
         35                  40                  45

Ile Tyr Gln Gly Lys Pro Tyr Tyr Phe Thr Trp Gly Tyr Ala Asp Ile
     50                  55                  60

Ala Lys Lys Gln Pro Val Thr Gln Gln Thr Leu Phe Glu Leu Gly Ser
 65                  70                  75                  80

Val Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg
                 85                  90                  95

Gly Glu Ile Lys Leu Ser Asp Pro Thr Thr Lys Tyr Trp Pro Glu Leu
            100                 105                 110

Thr Ala Lys Gln Trp Asn Gly Ile Thr Leu Leu His Leu Ala Thr Tyr
        115                 120                 125

Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu Val Lys Ser Ser

    130                 135                 140

Ser Asp Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Ala Trp Ala Pro
145                 150                 155                 160

Gly Thr Gln Arg Leu Tyr Ala Asn Ser Ser Ile Gly Leu Phe Gly Ala
                165                 170                 175

Leu Ala Val Lys Pro Ser Gly Leu Ser Phe Glu Gln Ala Met Gln Thr
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Arg Val Phe Gln Pro Leu Lys Leu Asn His Thr Trp Ile Asn Val Pro
        195                 200                 205

Pro Ala Glu Glu Lys Asn Tyr Ala Trp Gly Tyr Arg Glu Gly Lys Ala
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Val His Val Ser Pro Gly Ala Leu Asp Ala Glu Ala Tyr Gly Val Lys
225                 230                 235                 240

Ser Thr Ile Glu Asp Met Ala Arg Trp Val Gln Ser Asn Leu Lys Pro
                245                 250                 255

Leu Asp Ile Asn Glu Lys Thr Leu Gln Gln Gly Ile Gln Leu Ala Gln
            260                 265                 270

Ser Arg Tyr Trp Gln Thr Gly Asp Met Tyr Gln Gly Leu Gly Trp Glu
        275                 280                 285

Met Leu Asp Trp Pro Val Asn Pro Asp Ser Ile Ile Asn Gly Ser Asp
    290                 295                 300
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Asn Lys Ile Ala Leu Ala Ala Arg Pro Val Lys Ala Ile Thr Pro Pro
305 310 315 320

Thr Pro Ala Val Arg Ala Ser Trp Val His Lys Thr Gly Ala Thr Gly
325 330 335

Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys Glu Leu Gly Ile
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Val Met Leu Ala Asn Lys Asn Tyr Pro Asn Pro Ala Arg Val Asp Ala
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Ala Trp Gln Ile Leu Asn Ala Leu Gln
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<213> Escherichia coli

<220>
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<213> Bacillus licheniformis

<220>
<223> BlaR-CTD ß-lactamase

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Asp Tyr Ser Thr Phe Phe Asp Lys Phe Ser Ala Ser Gly Gly Phe Val
20 25 30

Leu Phe Asn Ser Asn Arg Lys Lys Tyr Thr Ile Tyr Asn Arg Lys Glu

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         35                  40                  45

Ser Thr Ser Arg Phe Ala Pro Ala Ser Thr Tyr Lys Val Phe Ser Ala
     50                  55                  60

Leu Leu Ala Leu Glu Ser Gly Ile Ile Thr Lys Asn Asp Ser His Met
 65                  70                  75                  80

Thr Trp Asp Gly Thr Gln Tyr Pro Tyr Lys Glu Trp Asn Gln Asp Gln
                 85                  90                  95

Asp Leu Phe Ser Ala Met Ser Ser Ser Thr Thr Trp Tyr Phe Gln Lys
            100                 105                 110

Leu Asp Arg Gln Ile Gly Glu Asp His Leu Arg His Tyr Leu Lys Ser
        115                 120                 125

Ile His Tyr Gly Asn Glu Asp Phe Ser Val Pro Ala Asp Tyr Trp Leu
    130                 135                 140

Asp Gly Ser Leu Gln Ile Ser Pro Leu Glu Gln Val Asn Ile Leu Lys
145                 150                 155                 160

Lys Phe Tyr Asp Asn Glu Phe Asp Phe Lys Gln Ser Asn Ile Glu Thr
                165                 170                 175

Val Lys Asp Ser Ile Arg Leu Glu Glu Ser Asn Gly Arg Val Leu Ser
            180                 185                 190

Gly Lys Thr Gly Thr Ser Val Ile Asn Gly Glu Leu His Ala Gly Trp
        195                 200                 205

Phe Ile Gly Tyr Val Glu Thr Ala Asp Asn Thr Phe Phe Phe Ala Val
    210                 215                 220

His Ile Gln Gly Glu Lys Arg Ala Ala Gly Ser Ser Ala Ala Glu Ile
225                 230                 235                 240

Ala Leu Ser Ile Leu Asp Lys Lys Gly Ile Tyr Pro Ser Val Ser Arg
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<400> 41

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tatacaatat acaataggaa agaaagcacc tccagattcg cacctgcttc cacctacaag 180
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gattattggc tggatggctc tcttcaaatt tctccacttg aacaggtcaa tatattaaaa 480
aagttttatg ataacgaatt tgattttaaa cagtctaata ttgaaactgt gaaagattcg 540
atacgtttag aagaatcaaa tggcagggtt ttatccggta aaaccggaac ctcggtaatc 600
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gcactttcca ttttagataa aaaagggatt tatccctccg tttcccga 768